NCBI ••••••••••••••••• Protein
[Sign In] [Register]
My NCBI

PubMed    Nucleotide    Protein    Genome    Structure    PMC    Taxonomy    OMIM    Books

Search Protein       for                                    Go  Clear

Display GenPept    Show 5    Send to

Range: from begin       to end       Features: ☐SNP [+]    Refresh

☐1: NP_059122. Reports nucleoporin 54kDa...[gi:26051237]                         BLink, Links

Comment  Features  Sequence

```
LOCUS       NP_059122               507 aa            linear   PRI 11-MAY-2008
DEFINITION  nucleoporin 54kDa [Homo sapiens].
ACCESSION   NP_059122
VERSION     NP_059122.2  GI:26051237
DBSOURCE    REFSEQ: accession NM_017426.2
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
REFERENCE   1  (residues 1 to 507)
  AUTHORS   Le Rouzic,E., Mousnier,A., Rustum,C., Stutz,F., Hallberg,E.,
            Dargemont,C. and Benichou,S.
  TITLE     Docking of HIV-1 Vpr to the nuclear envelope is mediated by the
            interaction with the nucleoporin hCG1
  JOURNAL   J. Biol. Chem. 277 (47), 45091-45098 (2002)
  PUBMED    12228227
REFERENCE   2  (residues 1 to 507)
  AUTHORS   Hu,R.M., Han,Z.G., Song,H.D., Peng,Y.D., Huang,Q.H., Ren,S.X.,
            Gu,Y.J., Huang,C.H., Li,Y.B., Jiang,C.L., Fu,G., Zhang,Q.H.,
            Gu,B.W., Dai,M., Mao,Y.F., Gao,G.F., Rong,R., Ye,M., Zhou,J.,
            Xu,S.H., Gu,J., Shi,J.X., Jin,W.R., Zhang,C.K., Wu,T.M.,
            Huang,G.Y., Chen,Z., Chen,M.D. and Chen,J.L.
  TITLE     Gene expression profiling in the human
            hypothalamus-pituitary-adrenal axis and full-length cDNA cloning
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9543-9548 (2000)
  PUBMED    10931946
REFERENCE   3  (residues 1 to 507)
  AUTHORS   Stoffler,D., Fahrenkrog,B. and Aebi,U.
  TITLE     The nuclear pore complex: from molecular architecture to functional
            dynamics
  JOURNAL   Curr. Opin. Cell Biol. 11 (3), 391-401 (1999)
  PUBMED    10395558
  REMARK    Review article
REFERENCE   4  (residues 1 to 507)
  AUTHORS   Bodoor,K., Shaikh,S., Enarson,P., Chowdhury,S., Salina,D.,
            Raharjo,W.H. and Burke,B.
  TITLE     Function and assembly of nuclear pore complex proteins
  JOURNAL   Biochem. Cell Biol. 77 (4), 321-329 (1999)
  PUBMED    10546895
  REMARK    Review article
REFERENCE   5  (residues 1 to 507)
  AUTHORS   Popov,S., Rexach,M., Ratner,L., Blobel,G. and Bukrinsky,M.
  TITLE     Viral protein R regulates docking of the HIV-1 preintegration
```

```
          complex to the nuclear pore complex
  JOURNAL   J. Biol. Chem. 273 (21), 13347-13352 (1998)
   PUBMED   9582382
REFERENCE   6  (residues 1 to 507)
  AUTHORS   Hu,T., Guan,T. and Gerace,L.
    TITLE   Molecular and functional characterization of the p62 complex, an
            assembly of nuclear pore complex glycoproteins
  JOURNAL   J. Cell Biol. 134 (3), 589-601 (1996)
   PUBMED   8707840
REFERENCE   7  (residues 1 to 507)
  AUTHORS   Finlay,D.R., Meier,E., Bradley,P., Horecka,J. and Forbes,D.J.
    TITLE   A complex of nuclear pore proteins required for pore function
  JOURNAL   J. Cell Biol. 114 (1), 169-183 (1991)
   PUBMED   2050741
COMMENT     REVIEWED REFSEQ: This record has been curated by NCBI staff. The
            reference sequence was derived from BC012559.1, AF157322.1 and
            BC034226.1.
            On Dec 5, 2002 this sequence version replaced gi:8393858.

            Summary: The nuclear envelope creates distinct nuclear and
            cytoplasmic compartments in eukaryotic cells. It consists of two
            concentric membranes perforated by nuclear pores, large protein
            complexes that form aqueous channels to regulate the flow of
            macromolecules between the nucleus and the cytoplasm. These
            complexes are composed of at least 100 different polypeptide
            subunits, many of which belong to the nucleoporin family. This gene
            encodes a member of the phe-gly (FG) repeat-containing nucleoporin
            subset.
FEATURES             Location/Qualifiers
     source          1..507
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="4"
                     /map="4q21.1"
     Protein         1..507
                     /product="nucleoporin 54kDa"
                     /note="nucleoporin p54"
                     /calculated_mol_wt=55305
     CDS             1..507
                     /gene="NUP54"
                     /coded_by="NM_017426.2:129..1652"
                     /db_xref="CCDS:CCDS3576.1"
                     /db_xref="GeneID:53371"
                     /db_xref="HGNC:17359"
                     /db_xref="HPRD:06352"
                     /db_xref="MIM:607607"
ORIGIN
        1 mafnfgapsg tsgtaaataa paggfggfgt tsttagsafs fsaptntggt glfggtqnkg
       61 fgfgtgfgtt tgtstglgtg lgtglgfggf ntqqqqqttl gglfsqptqa ptqsnqlint
      121 asalsaptll gderdailak wnqlqafwgt gkgyfnnnip pveftqenpf crfkavgysc
      181 mpsnkdedgl vvlvfnkket eirsqqqqlv eslhkvlggn qtltvnvegt ktlpddqtev
      241 viyvverspn gtsrrvpatt lyahfeqani ktqlqqlgvt lsmtrtelsp aqikqllqnp
      301 pagvdpiiwe qakvdnpdse klipvpmvgf kellrrlkvq dqmtkqhqtr ldiisedise
      361 lqknqttsva kiaqykrklm dlshrtlqvl ikqeiqrksg yaiqadeeql rvqldtiqge
      421 lnaptqfkgr lnelmsqirm qnhfgavrse eryyidadll reikqhlkqq qeglshlisi
      481 ikddledikl vehglnetih irggvfs
//
```

Search Protein           for

Display GenPept    Show 5    Send to

Range: from begin    to end    Features: [+]    Refresh

☐ 1: CAD97957. Reports hypothetical prot...[gi:31874087]                              BLink  Links

Comment  Features  Sequence

```
LOCUS       CAD97957                 291 aa            linear   PRI 17-JUN-2003
DEFINITION  hypothetical protein [Homo sapiens].
ACCESSION   CAD97957
VERSION     CAD97957.1  GI:31874087
DBSOURCE    embl accession BX538002.1
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
            Catarrhini; Hominidae; Homo.
REFERENCE   1  (residues 1 to 291)
  AUTHORS   Ansorge,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B.,
            Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
            Wiemann,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764
            Neuherberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by EMBL (European Molecular Biology Laboratories,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            This clone (DKFZp686B1269) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://mips.gsf.de/proj/cDNA/.
FEATURES             Location/Qualifiers
     source          1..291
                     /organism="Homo sapiens"
                     /db_xref="RZPD:DKFZp686B1269"
                     /db_xref="taxon:9606"
                     /map="4q21.1"
                     /clone="DKFZp686B1269"
                     /tissue_type="human endometrium carcinoma cell line"
                     /clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
                     DH10B; sites SfiIA + SfiIB"
                     /dev_stage="adult"
     Protein         1..291
                     /product="hypothetical protein"
     CDS             1..291
                     /gene="DKFZp686B1269"
                     /coded_by="BX538002.1:355..1230"
                     /note="nucleoporin p54 protein, differentially spliced"
```

```
                    /db_xref="GOA:Q7Z3B4"
                    /db_xref="HGNC:17359"
                    /db_xref="UniProtKB/Swiss-Prot:Q7Z3B4"
ORIGIN
        1 mpsnkdedgl vvlvfnkket eirsqqqqlv eslhkvlggn qtltvnvegt ktlpddqtev
       61 viyvverspn gtsrrvpatt lyahfeqani ktqlqqlgvt lsmtrtelsp aqikqllqnp
      121 pagvdpiiwe qakvdnpdse klipvpmvgf kellrrlkvq dqmtkqhqtr ldvlikqeiq
      181 rksgyaiqad eeqlrvqldt iqgelnaptq fkgrlnelms qirmqnhfga vrseeryyid
      241 adllreikqh lkqqqeglsh lisiikddle diklvehgln etihirggvf g
//
```

# NCBI Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

Matrix BLOSUM62  gap open: 11  gap extension: 1
x_dropoff: 0  expect: 300.000  wordsize: 3  Filter ☐  View option Standard
Masking character option X for protein, n for nucleotide ☐  Masking color option Black ☐
☐ Show CDS translation  [Align]

Sequence 1: gil31874087lhypothetical protein [Homo sapiens]
Length = 291 (1 .. 291)

Sequence 2: gil1537070lnucleoporin p54 [Rattus norvegicus] >gil8393855lreflNP_059057.1l nucleoporin
54kDa [Rattus norvegicus] >gil38257803lsplP70582lNUP54_RAT Nucleoporin p54 (54 kDa nucleoporin)
>gil50927635lgblAAH78858.1l Nucleoporin 54 [Rattus norvegicus] >gil149033843lgblEDL88639.1l
nucleoporin 54 [Rattus norvegicus]
Length = 510 (1 .. 510)
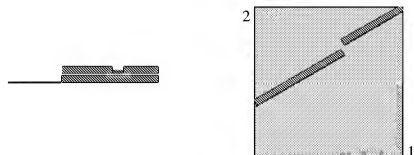


NOTE:Bitscore and expect value are calculated based on the size of the nr database.



```
 Score =  538 bits (1387),  Expect = 2e-151
 Identities = 281/326 (86%),  Positives = 288/326 (88%),  Gaps = 36/326 (11%)

Query  1    MPSNKDEDGLVVLVFNKKETEIRSQQQQLVESLHKVLGGNQTLTVNVEGTKTLPDDQTEV  60
            MP+NKDEDGLVVL+FNKKET+IRSQQQQLVESLHKVLGGNQTLTVNVEG KTLPDDQTEV
Sbjct  184  MPNNKDEDGLVVLIFNKKETDIRSQQQQLVESLHKVLGGNQTLTVNVEGIKTLPDDQTEV  243

Query  61   VIYVVERSPNGTSRRVPATTLYAHFEQANIKTQLQQLGVTLSMRTELSPAQIKQLLQNP   120
            VIY+VERSPNGTSRRVPATTLYAHFEQANIKTQLQQLGVTLSMRTELSPAQIKQLLQNP
Sbjct  244  VIYIVERSPNGTSRRVPATTLYAHFEQANIKTQLQQLGVTLSMRTELSPAQIKQLLQNP   303

Query  121  PAGVDPIIWEQAKVDNPDSEKLIPVPMVGFKELLRRLKVQDQMTKQHQTRLD--------  172
            PAGVDPIIWEQAKVDNPDSEKLIPVPMVGFKELLRRLKVQDQMTKQHQTRLD
Sbjct  304  PAGVDPIIWEQAKVDNPDSEKLIPVPMVGFKELLRRLKVQDQMTKQHQTRLDIISEDISE  363
```

```
Query  173  --------------------------VLIKQEIQRKSGYAIQADEEQLRVQLDTIQGE  204
                                      VLIKQEIQRKSGYAIQA+EEQLRVQLDTIQGE
Sbjct  364  LQKNQTTTMAKIAQYKRKLMDLSHRTLQVLIKQEIQRKSGYAIQAEEEQLRVQLDTIQGE  423

Query  205  LNAPTQFKGRLNELMSQIRMQNHFGAVRSEERYYIDADLLREIKQHLKQQQEGLSHLISI  264
            LNAPTQFKGRLNELMSQIRMQNHFGAV+SEE+YYIDADLLREIKQHLKQQQEGLSHLISI
Sbjct  424  LNAPTQFKGRLNELMSQIRMQNHFGAVKSEEKYYIDADLLREIKQHLKQQQEGLSHLISI  483

Query  265  IKDDLEDIKLVEHGLNETIHIRGGVF  290
            IKDDLEDIKLVEHGLNETIH RGGVF
Sbjct  484  IKDDLEDIKLVEHGLNETIHSRGGVF  509
```

```
CPU time:      0.04 user secs.       0.03 sys. secs       0.07 total secs.
```